Phenotypic and Genotypic characterization of Vancomycin resistant *Staphylococcus aureus* among MRSA isolates in a tertiary care hospital.

Abstract:

MRSA is one of the most important etiology of community and hospital acquired infections. With the increasing incidence of Methicillin resistant *Staphylococcus aureus*(MRSA), Vancomycin intermediate *Staphylococcus aureus* (VISA) & Vancomycin resistant *Staphylococcus aureus* (VRSA) strains are not a rare phenomenon nowadays. Emergence of VISA and VRSA strains has led to a great concern in global public health in both developed and developed countries. The aim of the present study was to determine the prevalence of of Vancomycin resistant *Staphylococcus aureus* strains among MRSA isolates and their antibiotic susceptibility pattern in Tirunelveli Medical College Hospital between July 2017 to July 2018. In this prospective cross sectional study, 100 *Staphylococcus aureus* were isolated and identified conventionally from various clinical specimens collected from different departments of the hospital. Subsequently, antimicrobial susceptibility test was performed by Kirby Bauer disk diffusion method as per Clinical and Laboratory Standards Institute (CLSI) guidelines. Among the 100 *S.aureus* isolates, MRSA was found to be 54% by Cefoxitin(30 μg) disk diffusion method. And among the 54% of the MRSA strains isolated 1 (1.85%) was VISA and 1 (1.85%) was VRSA with MIC 4 and 16 respectively as detected by E Test (Hi Media,Mumbai).Both the strains were found to be 100% sensitive to glycopeptides Linezolid and Teicoplanin which are the currently available drugs for treatment of VRSA infections.Both the isolates were subjected to Polymerase chain Reaction by Agarose Gel Electrophoresis, but *Van A* gene was not detected. This can be implicated by the fact that VISA is due to thickened cell wall which contributed to resistance and the resistance mechanism in VRSA strain might be due to genes other than *Van A* gene. Though the incidence of VISA and VRSA are relatively less,it just represents the tip of the ice berg. Hence, larger studies need to be done in various geographical regions of the country to better define the epidemiology, mechanism of Vancomycin resistance and its clinical implications.

Keywords - MRSA, VISA, VRSA, E test, MIC, *Van A* gene, PCR